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### 1 [Probabilistic discovery of overlapping cellular processes and their regulation](#)

Alexis Battle, Eran Segal, Daphne Koller

 March 2004 **Proceedings of the eighth annual international conference on Computational molecular biology**

 Full text available: [pdf\(259.52 KB\)](#) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Many of the functions carried out by a living cell are regulated at the transcriptional level, to ensure that genes are expressed when they are needed. Thus, to understand biological processes, it is thus necessary to understand the cell's transcriptional network. In this paper, we propose a novel probabilistic model of gene regulation for the task of identifying overlapping biological processes and the regulatory mechanism controlling their activation. A key feature of our approach is that we a ...

**Keywords:** cellular processes, gene regulation, probabilistic relational models

### 2 [From informatics to bioinformatics](#)

Vladimir B. Bajic, Vladimir Brusic, Jinyan Li, See-Kiong Ng, Limsoon Wong

 January 2003 **Proceedings of the First Asia-Pacific bioinformatics conference on Bioinformatics 2003 - Volume 19**

 Full text available: [pdf\(538.23 KB\)](#) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Informatics has helped in launching molecular biology into the genomic era. It appears certain that informatics will continue to be a major factor in the success of molecular biology in the post-genome era. In this paper, we describe advances made in data integration and data mining technologies that are relevant to molecular biology and biomedical sciences. In particular, we discuss some past and present research results on topics such as (a) the taming of autonomous heterogeneous distributed d ...

**Keywords:** Dragon, FIMM, Kleisli, PCL, PIES, bioinformatics, data integration, data warehousing, epitope prediction, gene expression analysis, protein interaction extraction, transcription start site recognition

### 3 [IS consultants and the change agent role](#)

Elaine R. Winston

 October 1999 **ACM SIGCPR Computer Personnel**, Volume 20 Issue 4

Full text available:  pdf(1.66 MB)Additional Information: [full citation](#), [abstract](#), [references](#)

Markus and Benjamin (1996) proposed a change agency model that identifies three change agent roles for the information system (IS) specialist: the traditional, the facilitator, and the advocator. This study explores these roles for IS consultants who are engaged as independent contractors by small businesses. Presented here is a field study of twenty-five cases to test these three roles. In general, the results of the study suggest that IS consultants' view themselves as change agents and can i ...

**Keywords:** case study, change management, is personnel, research methodology, resistance to change

#### 4 [Industry track papers: Handling very large numbers of association rules in the analysis of microarray data](#)

Alexander Tuzhilin, Gediminas Adomavicius

July 2002 **Proceedings of the eighth ACM SIGKDD international conference on Knowledge discovery and data mining**Full text available:  pdf(953.83 KB)Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

The problem of analyzing microarray data became one of important topics in bioinformatics over the past several years, and different data mining techniques have been proposed for the analysis of such data. In this paper, we propose to use association rule discovery methods for determining associations among expression levels of different genes. One of the main problems related to the discovery of these associations is the scalability issue. Microarrays usually contain very large numbers of genes ...

**Keywords:** analysis of microarray data, association rules, bioinformatics, expert-driven rule validation, post-processing of discovered rules, rule filtering, rule grouping

#### 5 [Requirements interaction management](#)

William N. Robinson, Suzanne D. Pawlowski, Vecheslav Volkov

June 2003 **ACM Computing Surveys (CSUR)**, Volume 35 Issue 2Full text available:  pdf(1.24 MB)Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Requirements interaction management (RIM) is the set of activities directed toward the discovery, management, and disposition of critical relationships among sets of requirements, which has become a critical area of requirements engineering. This survey looks at the evolution of supporting concepts and their related literature, presents an issues-based framework for reviewing processes and products, and applies the framework in a review of RIM state-of-the-art. Finally, it presents seven research ...

**Keywords:** KAOS, KATE, Oz, Requirements engineering, Telos, WinWin, analysis and design, composite system, deficiency driven design, dependency analysis, distributed intentionality, interaction analysis, software cost reduction (SCR), system architecture, system specification, viewpoints

#### 6 [A multi-agent architecture for process management accommodates unexpected performance](#)

John Debenham

March 2000 **Proceedings of the 2000 ACM symposium on Applied computing**Full text available:  pdf(1.00 MB)Additional Information: [full citation](#), [references](#), [index terms](#)

**Keywords:** business process management, multi-agent systems

7 Phylogenetically and spatially conserved word pairs associated with gene expression changes in yeasts

Derek Y. Chiang, Alan M. Moses, Manolis Kamvysselis, Eric S. Lander, Michael B. Eisen  
April 2003 **Proceedings of the seventh annual international conference on Computational molecular biology**

Full text available:  pdf(1.26 MB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

**Background.** Transcriptional regulation in eukaryotes is often multifactorial, involving multiple transcription factors binding to the same transcription control region (e.g., upstream activating sequences and enhancers), and to understand the regulatory content of eukaryotic genomes it is necessary to consider the co-occurrence and spatial relationships of individual binding sites. The identification of sequences conserved among related species (often known as phylogenetic footprinting) h ...

**Keywords:** comparative genomics, multifactorial regulation, phylogenetic footprinting, promoter structure, transcription regulation

8 Articles on microarray data mining: Towards interactive exploration of gene expression patterns

Daxin Jiang, Jian Pei, Aidong Zhang  
December 2003 **ACM SIGKDD Explorations Newsletter**, Volume 5 Issue 2

Full text available:  pdf(527.68 KB) Additional Information: [full citation](#), [abstract](#), [references](#)

Analyzing coherent gene expression patterns is an important task in bioinformatics research and biomedical applications. Recently, various clustering methods have been adapted or proposed to identify clusters of co-expressed genes and recognize coherent expression patterns as the centroids of the clusters. However, the interpretation of co-expressed genes and coherent patterns mainly depends on the domain knowledge, which presents several challenges for coherent pattern mining and cannot be solv ...

9 Integration of various emotion eliciting factors for life-like agents

Kwangyong Lee  
October 1999 **Proceedings of the seventh ACM international conference on Multimedia (Part 2)**

Full text available:  pdf(462.41 KB) Additional Information: [full citation](#), [references](#), [index terms](#)

**Keywords:** emotion eliciting factors, emotion generation, lifelike agents

10 Reasoning about knowledge and probability


Ronald Fagin, Joseph Y. Halpern  
March 1994 **Journal of the ACM (JACM)**, Volume 41 Issue 2

Full text available:  pdf(2.23 MB) Additional Information: [full citation](#), [references](#), [citations](#), [index terms](#), [review](#)

**Keywords:** knowledge, modal logic, nondeterminism vs. probability, possible worlds, probabilistic common knowledge, probabilistic knowledge, reasoning about knowledge and probability

**11 Multi-Agent Organisms for Persistent Computing**

Kenneth N. Lodding, Paul Brewster

July 2004 **Proceedings of the Third International Joint Conference on Autonomous Agents and Multiagent Systems - Volume 3**Full text available:  pdf(218.33 KB) Additional Information: [full citation](#), [abstract](#)

The defining characteristic of a multicellular organism is unity of purpose. In biology, the purpose is survival of the organism. The purpose of our multi-agent system is to provide a persistent computing environment in harsh conditions where repairs are difficult, or impossible. The multi-agent organism is a single entity built from logically dependent cells, where each cell is a discrete, independent hardware-processing unit. Similar to biology, each cell contains a full description of the sys ...

**12 Evaluating the Modeling and Use of Emotion in Virtual Humans**

Jonathan Gratch, Stacy Marsella

July 2004 **Proceedings of the Third International Joint Conference on Autonomous Agents and Multiagent Systems - Volume 1**Full text available:  pdf(331.35 KB) Additional Information: [full citation](#), [abstract](#)

Spurred by a range of potential applications, there has been a growing body of research in computational models of human emotion. To advance the development of these models, it is critical that we begin to evaluate them against the phenomena they purport to model. In this paper, we present one methodology to evaluate an emotion model. The methodology is based on comparing the behavior of the computational model against human behavior, using a standard clinical instrument for assessing human emot ...

**13 Full Technical Papers: Inferring user goals from personality and behavior in a causal model of user affect**

Xiaoming Zhou, Cristina Conati

January 2003 **Proceedings of the 8th international conference on Intelligent user interfaces**Full text available:  pdf(700.99 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

We present a probabilistic model, based on Dynamic Decision Networks, to assess user affect from possible causes of emotional arousal. The model relies on the OCC cognitive theory of emotions and is designed to assess student affect during the interaction with an educational game. A key element of applying the OCC theory to assess user affect is knowledge of user goals. Thus, in this paper we focus on describing how our model infers these goals from user personality traits and interaction behavi ...

**Keywords:** affective computing, dynamic decision networks, educational games, user modeling

**14 Discovery of multi-level rules and exceptions from a distributed database**


Rónán Páircéir, Sally McClean, Bryan Scotney

August 2000 **Proceedings of the sixth ACM SIGKDD international conference on Knowledge discovery and data mining**Full text available:  pdf(132.32 KB) Additional Information: [full citation](#), [references](#), [index terms](#)

**Keywords:** aggregates, distributed databases, exception discovery, multi-level statistical models, rule discovery, sufficient statistics

**15 Inferring domain-domain interactions from protein-protein interactions**


Minghua Deng, Shipra Mehta, Fengzhu Sun, Ting Chen

April 2002 **Proceedings of the sixth annual international conference on Computational biology**Full text available:  [pdf\(1.95 MB\)](#)Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

Protein-protein interactions are important events in cellular and biochemical processes within a cell. Several researchers have undertaken the task of analyzing protein-protein interactions covering all genes of an organism by using yeast two-hybrid assays. Protein-protein interactions involve physical interactions between protein domains. Therefore, understanding protein interactions at the domain level gives a global view of the protein interaction network, and possibly extends functions of pr ...

**16 Poster papers: Collusion in the U.S. crop insurance program: applied data mining**


Bertis B. Little, Walter L. Johnston, Ashley C. Lovell, Roderick M. Rejesus, Steve A. Steed

July 2002 **Proceedings of the eighth ACM SIGKDD international conference on Knowledge discovery and data mining**Full text available:  [pdf\(450.56 KB\)](#)Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

This paper quantitatively analyzes indicators of Agent (policy seller), Adjuster (indemnity claim adjuster), Producer (policy purchaser/holder) indemnity behavior suggestive of collusion in the United States Department of Agriculture (USDA) Risk Management Agency (RMA) national crop insurance program. According to guidance from the federal law and using six indicator variables of indemnity behavior, those entities equal to or exceeding 150% of the county mean (computed using a simple jackknife p ...

**Keywords:** collusion, doublets, insurance fraud, log linear models, non-recursive, triplets**17 Articles on microarray data mining: Differential expression, class discovery and class prediction using S-PLUS and S+ArrayAnalyzer**

Michael O'Connell

December 2003 **ACM SIGKDD Explorations Newsletter**, Volume 5 Issue 2Full text available:  [pdf\(958.46 KB\)](#)Additional Information: [full citation](#), [abstract](#), [references](#)

Microarrays are a powerful experimental platform, allowing simultaneous studies of gene expression for thousands of genes under different experimental conditions. However there is much biological variability induced throughout the experimental process that can obscure the biological signals of interest. As such, the need for experimental design, replication and statistical rigor are now widely recognized. Statistical hypothesis testing has become the accepted differential expression analysis app ...

**Keywords:** S+ArrayAnalyzer, S-PLUS, class discovery, class prediction, differential expression**18 Special topic section on peer to peer data management: Relational data sharing in peer-based data management systems**

Beng Chin Ooi, Yanfeng Shu, Kian-Lee Tan

September 2003 **ACM SIGMOD Record**, Volume 32 Issue 3Full text available:  [pdf\(69.76 KB\)](#)Additional Information: [full citation](#), [abstract](#), [references](#)


Data sharing in current P2P systems is very much restricted to file-system-like capabilities.

In this paper, we present the strategies that we have adopted in our BestPeer project to support more fine-grained data sharing, especially, relational data sharing, in a P2P context. First, we look at some of the issues in designing a peer-based data management system, and discuss some possible solutions to address these issues. Second, we present the design of our first prototype system, PeerDB, and r ...

#### 19 Oracle's technology for bioinformatics and future directions

Bruce Blackwell, Siva Ravada

January 2003 **Proceedings of the First Asia-Pacific bioinformatics conference on Bioinformatics 2003 - Volume 19**

Full text available:  pdf(74.48 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)


The Oracle relational database management system, with object-oriented extensions and numerous application-driven enhancements, plays a critical role worldwide in managing the exploding volumes of bioinformatics data. There are many features of the Oracle product which support the bioinformatics community directly already and there are several features that could be exploited more thoroughly by users, service vendors, and Oracle itself to extend that level of support. This paper will present an ...

**Keywords:** bioinformatics, database, extensibility, oracle

#### 20 The management of end-user computing: status and directions

James C. Brancheau, Carol V. Brown

December 1993 **ACM Computing Surveys (CSUR)**, Volume 25 Issue 4

Full text available:  pdf(3.74 MB) Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

The development of computing applications by the people who have direct need for them in their work has become commonplace. During the 1980s, development of applications by "end users" accelerated and became a key management and research concern. Known as "end-user computing," the phenomena and research associated with this trend cross a variety of disciplines. This article critically surveys the published literature on end-user computing (EUC) management according to ...

**Keywords:** desktop computing, end-user computing, information center, information technology management, personal computing

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Sara C. Madeira, Arlindo L. Oliveira

January 2004 **IEEE/ACM Transactions on Computational Biology and Bioinformatics****(TCBB)**, Volume 1 Issue 1Full text available: [pdf\(1.28 MB\)](#)Additional Information: [full citation](#)

**Keywords:** Biclustering, simultaneous clustering, coclustering, subspace clustering, bidimensional clustering, direct clustering, block clustering, two-way clustering, two-mode clustering, two-sided clustering, microarray data analysis, biological data analysis, gene expression data.

**22 [Of parts and relationships: an unending quest](#)**

Isidore Rigoutsos

November 2004 **Proceedings of the Thirteenth ACM conference on Information and knowledge management**Full text available: [pdf\(114.26 KB\)](#)Additional Information: [full citation](#), [abstract](#)

Systems biology is a field which focuses on the interpretation of large, diverse sets of biological measurements in order to elucidate the complex mechanisms that underly important and (seemingly simple) macroscopic phenotypes. The problem at hand is hierarchical in nature, with the hierarchy spanning many levels. Each of these levels can be thought of as comprising multiple active agents that are diverse in their nature (e.g. genes, proteins, pathways, organelles, etc) and also in their beha ...


**23 [A proposal for valuing information and instrumental goods](#)**

Marshall V. Van Alstyne

January 1999 **Proceeding of the 20th international conference on Information Systems**Full text available: [pdf\(405.51 KB\)](#)Additional Information: [full citation](#), [references](#), [index terms](#)**24 [Probabilistic hierarchical clustering for biological data](#)**

Eran Segal, Daphne Koller

April 2002 **Proceedings of the sixth annual international conference on Computational**

**biology**Full text available:  [pdf\(2.06 MB\)](#)Additional Information: [full citation](#), [abstract](#), [citations](#), [index terms](#)

Biological data, such as gene expression profiles or protein sequences, is often organized in a hierarchy of classes, where the instances assigned to "nearby" classes in the tree are similar. Most approaches for constructing a hierarchy use simple local operations, that are very sensitive to noise or variation in the data. In this paper, we describe probabilistic abstraction hierarchies (PAH) [11], a general probabilistic framework for clustering data into a hierarchy, and show how it can be app ...

## 25 Distributed awareness in MAS: Minimizing communication cost in a distributed Bayesian network using a decentralized MDP

Jiaying Shen, Victor Lesser, Norman Carver

July 2003 **Proceedings of the second international joint conference on Autonomous agents and multiagent systems**Full text available:  [pdf\(209.97 KB\)](#)Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

In complex distributed applications, a problem is often decomposed into a set of subproblems that are distributed to multiple agents. We formulate this class of problems with a two layer Bayesian Network. Instead of merely providing a statistical view, we propose a satisficing approach to predict the minimum expected communication needed to reach a desired solution quality. The problem is modelled with a decentralized MDP, and two approximate algorithms are developed to find the near optimal com ...

**Keywords:** Bayesian networks, action selection, coordination of multiple agents, decentralized MDPs, decision-theoretic planning

## 26 Bias-Variance Analysis of Support Vector Machines for the Development of SVM-Based Ensemble Methods

Giorgio Valentini, Thomas G. Dietterich

August 2004 **The Journal of Machine Learning Research**, Volume 5Full text available:  [pdf\(2.41 MB\)](#)Additional Information: [full citation](#), [abstract](#)

Bias-variance analysis provides a tool to study learning algorithms and can be used to properly design ensemble methods well tuned to the properties of a specific base learner. Indeed the effectiveness of ensemble methods critically depends on accuracy, diversity and learning characteristics of base learners. We present an extended experimental analysis of bias-variance decomposition of the error in Support Vector Machines (SVMs), considering Gaussian, polynomial and dot product kernels. A chara ...

## 27 Bug isolation via remote program sampling

Ben Liblit, Alex Aiken, Alice X. Zheng, Michael I. Jordan


May 2003 **ACM SIGPLAN Notices , Proceedings of the ACM SIGPLAN 2003 conference on Programming language design and implementation**, Volume 38 Issue 5Full text available:  [pdf\(258.37 KB\)](#)Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

We propose a low-overhead sampling infrastructure for gathering information from the executions experienced by a program's user community. Several example applications illustrate ways to use sampled instrumentation to isolate bugs. Assertion-dense code can be transformed to share the cost of assertions among many users. Lacking assertions, broad guesses can be made about predicates that predict program errors and a process of elimination used to whittle these down to the true bug. Finally, even ...

**Keywords:** assertions, bug isolation, feature selection, logistic regression, random sampling, statistical debugging

**28 Automatic segmentation of text into structured records**

Vinayak Borkar, Kaustubh Deshmukh, Sunita Sarawagi

May 2001 **ACM SIGMOD Record , Proceedings of the 2001 ACM SIGMOD international conference on Management of data**, Volume 30 Issue 2Full text available:  pdf(331.70 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

In this paper we present a method for automatically segmenting unformatted text records into structured elements. Several useful data sources today are human-generated as continuous text whereas convenient usage requires the data to be organized as structured records. A prime motivation is the warehouse address cleaning problem of transforming dirty addresses stored in large corporate databases as a single text field into subfields like "City" and "Street". Existing to ...

**29 Dynamical systems trees**

Andrew Howard, Tony Jebara

July 2004 **Proceedings of the 20th conference on Uncertainty in artificial intelligence**Full text available:  pdf(597.74 KB) Additional Information: [full citation](#), [abstract](#), [references](#)

We propose dynamical systems trees (DSTs) as a flexible class of models for describing multiple process that interact via a hierarchy of aggregating parent chains. DSTs extend Kalman filters, hidden Markov models and nonlinear dynamical systems to an interactive group scenario. Various individual processes interact as communities and sub-communities in a tree structure that is unrolled in time. To accommodate nonlinear temporal activity, each individual leaf process is modeled as a dynamical ...

**30 Gaining insights into support vector machine pattern classifiers using projection-based tour methods**

Doina Caragea, Dianne Cook, Vasant G. Honavar

August 2001 **Proceedings of the seventh ACM SIGKDD international conference on Knowledge discovery and data mining**Full text available:  pdf(528.22 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

This paper discusses visual methods that can be used to understand and interpret the results of classification using support vector machines (SVM) on data with continuous real-valued variables. SVM induction algorithms build pattern classifiers by identifying a maximal margin separating hyperplane from training examples in high dimensional pattern spaces or spaces induced by suitable nonlinear kernel transformations over pattern spaces. SVM have been demonstrated to be quite effective in a number ...

**Keywords:** Dynamic graphics, classification, machine learning, multivariate data, support vector machines, tours, visualization

**31 Keynote address: Visualization challenges for a new cyberpharmaceutical computing paradigm**

Russell J. Turner, Kabir Chaturvedi, Nathan J. Edwards, Daniel Fasulo, Aaron L. Halpern, Daniel H. Huson, Oliver Kohlbacher, Jason R. Miller, Knut Reinert, Karin A. Remington, Russell Schwartz, Brian Walenz, Shibu Yooseph, Sorin Istrail

October 2001 **Proceedings of the IEEE 2001 symposium on parallel and large-data visualization and graphics**Full text available:  pdf(3.07 MB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

In recent years, an explosion in data has been profoundly changing the field of biology and creating the need for new areas of expertise, particularly in the handling of data. One vital area that has so far received insufficient attention is how to communicate the large

quantities of diverse and complex information that is being generated. Celera has encountered a number of visualization problems in the course of developing tools for bioinformatics research, applying them to our data generation ...

32 Data engineering for life sciences: Using reasoning to guide annotation with gene ontology terms in GOAT

Michael Bada, Daniele Turi, Robin McEntire, Robert Stevens

June 2004 **ACM SIGMOD Record**, Volume 33 Issue 2

Full text available:  pdf(2.14 MB) Additional Information: [full citation](#), [abstract](#), [references](#)

High-quality annotation of biological data is central to bioinformatics. Annotation using terms from ontologies provides reliable computational access to data. The Gene Ontology (GO), a structured controlled vocabulary of nearly 17,000 terms, is becoming the *de facto* standard for describing the functionality of gene products. Many prominent biomedical databases use GO as a source of terms for functional annotation of their gene-product entries to promote consistent querying and interoperability ...

33 Mapping the physical world to psychological reality: creating synthetic environments

Ronald W. Noel, Claudia M. Hunter

August 2000 **Proceedings of the conference on Designing interactive systems: processes, practices, methods, and techniques**

Full text available:  pdf(432.45 KB) Additional Information: [full citation](#), [abstract](#), [references](#)

The successful creation of telepresence and virtual environments requires a change in design paradigm. We must move away from attempts to recreate reality in its entirety toward the creation of environments that are psychologically real for humans, because in fact, reality mediated through display devices is largely subjective. The experiments discussed in this paper show that a single intrinsic physical property, such as the velocity or stability of a vehicle, can give rise to a multitude of ...

**Keywords:** design paradigms, display semantics, speed perception, synthetic environments, telepresence, virtual reality

34 Probability and uncertainty: Epistemology probabilized

Richard Jeffrey

July 2001 **Proceedings of the 8th conference on Theoretical aspects of rationality and knowledge**

Full text available:  pdf(780.14 KB) Additional Information: [full citation](#), [abstract](#), [references](#)

Here is a framework for judgment in terms of a continuum of "subjective" probabilities, a framework in which probabilistic judgments need not stand on a foundation of certainties. In place of propositional data bases, this *radical* probabilism ("probabilities all the way down to the roots") envisages full or partial probability assignments to probability spaces, together with protocols for revising those assignments and their interconnections in the light of fresh empirical or ...

35 DEADLINER: building a new niche search engine

A. Kruger, C. L. Giles, F. M. Coetzee, E. Glover, G. W. Flake, S. Lawrence, C. Omlin

November 2000 **Proceedings of the ninth international conference on Information and knowledge management**

Full text available:  pdf(340.59 KB) Additional Information: [full citation](#), [references](#), [citations](#), [index terms](#)

**Keywords:** Bayesian fusion approaches, text extraction, web search

### 36 The virtual design team

John C. Kunz, Tore R. Christiansen, Geoff P. Cohen, Yan Jin, Raymond E. Levitt  
November 1998 **Communications of the ACM**, Volume 41 Issue 11

Full text available:  pdf(368.19 KB) Additional Information: [full citation](#), [references](#), [citations](#), [index terms](#), [review](#)



### 37 A bayesian approach to transcript estimation from gene array data: the BEAM technique

Ron O. Dror, Jonathan G. Murnick, Nicola A. Rinaldi, Voichita D. Marinescu, Ryan M. Rifkin, Richard A. Young  
April 2002 **Proceedings of the sixth annual international conference on Computational biology**

Full text available:  pdf(1.84 MB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

We present a new statistically optimal approach to estimate transcript levels and ratios from one or more gene array experiments. The Bayesian Estimation of Array Measurements (BEAM) technique uses a model of measurement noise and prior information to estimate biological expression levels. It provides a principled method to deal with negative expression level measurements, combine multiple measurements, and identify changes in expression level. BEAM is more flexible than existing techniques, bec ...

**Keywords:** DNA microarrays, affymetrix chips, bayesian estimation, statistical confidence



### 38 Long papers: recommendation and instruction: Improving proactive information systems

Daniel Billsus, David M. Hilbert, Dan Maynes-Aminzade  
January 2005 **Proceedings of the 10th international conference on Intelligent user interfaces**

Full text available:  pdf(833.30 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Proactive contextual information systems help people locate information by automatically suggesting potentially relevant resources based on their current tasks or interests. Such systems are becoming increasingly popular, but designing user interfaces that effectively communicate recommended information is a challenge: the interface must be unobtrusive, yet communicate enough information at the right time to provide value to the user. In this paper we describe our experience with the FXPAL Bar, ...

**Keywords:** agents, context, proactive recommendations



### 39 Business models and market mechanisms: evaluating efficiencies in consumer electronic markets

Jonathan Palmer, Markus Lindemann  
June 2003 **ACM SIGMIS Database**, Volume 34 Issue 2

Full text available:  pdf(287.67 KB) Additional Information: [full citation](#), [abstract](#), [references](#)

The paper examines business models utilizing three different market mechanisms on the Internet: direct search, broker, and dealer. Utilizing capital markets and information theory to compare the business models, the research looks at specific market mechanisms instantiated in PriceScan, NetMarket, and Bottom Dollar. The web sites supporting the market structures were also evaluated on trust mechanisms, reputational ratings, information quality, availability, speed, and liquidity. Twenty standard ...



**Keywords:** efficiency, electronic markets, market structure, world wide web

40 Employment outsourcing in information systems

Sandra Slaughter, Soon Ang

July 1996 **Communications of the ACM**, Volume 39 Issue 7

Full text available:  [pdf\(304.68 KB\)](#)

Additional Information: [full citation](#), [references](#), [citations](#), [index terms](#)



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Best 200 shown

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#### 41 [Integrated visualization of brain anatomy and cerebral blood vessels](#)

Dirk Vandermeulen, Peter Plets, Steven Ramkers, Paul Suetens, Guy Marchal

 December 1992 **Proceedings of the 1992 workshop on Volume visualization**

 Full text available: [pdf\(1.02 MB\)](#)

 Additional Information: [full citation](#), [references](#), [index terms](#)

#### 42 [Surveys: Integration of biological sources: current systems and challenges ahead](#)

Thomas Hernandez, Subbarao Kambhampati

 September 2004 **ACM SIGMOD Record**, Volume 33 Issue 3

 Full text available: [pdf\(78.41 KB\)](#)

 Additional Information: [full citation](#), [abstract](#), [references](#)

This paper surveys the area of biological and genomic sources integration, which has recently become a major focus of the data integration research field. The challenges that an integration system for biological sources must face are due to several factors such as the variety and amount of data available, the representational heterogeneity of the data in the different sources, and the autonomy and differing capabilities of the sources.

This survey describes the main integration approach ...

#### 43 [Regular papers: Clustering verbs semantically according to their alternation behaviour](#)

Sabine Schulte im Walde

 July 2000 **Proceedings of the 17th conference on Computational linguistics - Volume 2**

 Full text available: [pdf\(615.19 KB\)](#)

 Additional Information: [full citation](#), [abstract](#), [references](#)

Verbs were clustered semantically on the basis of their alternation behaviour, as characterised by their syntactic subcategorisation frames extracted from maximum probability parses of a robust statistical parser, and completed by assigning WordNet classes as selectional preferences to the frame arguments. The clustering was achieved (a) iteratively by measuring the relative entropy between the verbs' probability distributions over the frame types, and (b) by utilising a latent class analysis ba ...

#### 44 [Measuring user involvement: a diffusion of innovation perspective](#)

Leon A. Kappelman

 May 1995 **ACM SIGMIS Database**, Volume 26 Issue 2-3

 Full text available: [pdf\(1.54 MB\)](#)

 Additional Information: [full citation](#), [abstract](#), [citations](#), [index terms](#)

User involvement is a need-based motivational attitude toward information systems and their development. As such, it has important implications for the successful creation and deployment of information systems in organizations. This paper reports on the development and validation of an instrument to determine if the distinction between a user's involvement in the process of information system diffusion can be measured independently of that user's involvement with the information system innovatio ...

**Keywords:** adaptation, attitude, diffusion of innovation, implementation, instrument validation, research frameworks, research methods, user engagement, user involvement, user participation, user process involvement, user satisfaction, user system involvement

45 Reports: Report on the 18<sup>th</sup> British National Conference on Databases (BNCOD)

Carole Goble, Brian Read

March 2002 **ACM SIGMOD Record**, Volume 31 Issue 1

Full text available:  [pdf\(303.80 KB\)](#) Additional Information: [full citation](#), [abstract](#)

The annual series of the British National Conference on Databases has been a forum for UK database practitioners and a focus for database research since 1981. In recent years, interest in this conference series has extended well beyond the UK. BNCOD 2001, the 18th conference in the series, was held at the CLRC Rutherford Appleton Laboratory (RAL) from 9th -11th July 2001. RAL hosts national large-scale facilities for advanced scientific research. The Information Technology Department collaborates ...

46 The influence of persuasion, training and experience on user perceptions and acceptance of IT innovation

Weidong Xia, Gwanhoo Lee

December 2000 **Proceedings of the twenty first international conference on Information systems**

Full text available:  [pdf\(142.13 KB\)](#) Additional Information: [full citation](#), [references](#), [citations](#), [index terms](#)

47 Special issue on on inductive logic programming: Ilp: a short look back and a longer look forward

David Page, Ashwin Srinivasan

December 2003 **The Journal of Machine Learning Research**, Volume 4

Full text available:  [pdf\(103.21 KB\)](#) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Inductive logic programming (ILP) is built on a foundation laid by research in machine learning and computational logic. Armed with this strong foundation, ILP has been applied to important and interesting problems in the life sciences, engineering and the arts. This paper begins by briefly reviewing some example applications, in order to illustrate the benefits of ILP. In turn, the applications have brought into focus the need for more research into specific topics. We enumerate and elaborate f ...

48 Learning multiple evolutionary pathways from cross-sectional data

Niko Beerenwinkel, Jörg Rahnenführer, Martin Däumer, Daniel Hoffmann, Rolf Kaiser, Joachim Selbig, Thomas Lengauer

March 2004 **Proceedings of the eighth annual international conference on Computational molecular biology**

Full text available:  [pdf\(193.60 KB\)](#) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

We introduce a mixture model of trees to describe evolutionary processes that are characterized by the accumulation of permanent genetic changes. The basic building block of the model is a directed weighted tree that generates a probability distribution on the set




of all patterns of genetic events. We present an EM-like algorithm for learning a mixture model of  $K$  trees and show how to determine  $K$  with a maximum likelihood approach. As a case study we consider the accumulation of mu ...

**Keywords:** EM algorithm, HIV drug resistance, bayesian networks, mixture models, mutational pathways, tree models

#### 49 Commitment development in software process improvement: critical misconceptions

Pekka Abrahamsson

July 2001 **Proceedings of the 23rd International Conference on Software Engineering**

Full text available:  pdf(158.09 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

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*It has been well established in the software process improvement (SPI) literature and practice that without commitment from all organizational levels to SPI the initiative will most likely fail or the results are not far reaching. Commitment construct is explored and three forms of commitment are introduced: affective, continuance and normative commitment. Analysis shows that current models of commitment development lack scientific validity and are based on four misconceptions: (1) the ass ...*

**Keywords:** commitment, commitment models, forms of commitment, misconceptions, software process improvement

#### 50 Adaptive Energy Conservation Model using Dynamic Caching for Wireless Devices

Constandinos X. Mavromoustakis, Helen D. Karatza

April 2004 **Proceedings of the 37th annual symposium on Simulation**

Full text available:  pdf(161.01 KB) Additional Information: [full citation](#), [abstract](#)

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One important issue that has to be taken into account in wireless devices is the energy conservation. Every infrastructureless network must be adaptively selfconfigured particularly in terms of energy, connectivity, and memory. Efficient utilization of battery power is important for wireless users because due to their movements their energy is fluctuating at different levels during operation mode. Traffic plays a major role for energy consumption because of the unpredictable incoming-flow nature. This p ...

#### 51 Structural ambiguity and lexical relations

Donald Hindle, Mats Rooth

June 1991 **Proceedings of the 29th conference on Association for Computational Linguistics**

Full text available:  pdf(699.00 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#)

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We propose that ambiguous prepositional phrase attachment can be resolved on the basis of the relative strength of association of the preposition with noun and verb, estimated on the basis of word distribution in a large corpus. This work suggests that a distributional approach can be effective in resolving parsing problems that apparently call for complex reasoning.

#### 52 On the relationship between strand spaces and multi-agent systems

Joseph Y. Halpern, Riccardo Pucella

February 2003 **ACM Transactions on Information and System Security (TISSEC)**, Volume 6 Issue 1

Full text available:  pdf(248.91 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#), [review](#)

*Strand spaces* are a popular framework for the analysis of security protocols. Strand spaces have some similarities to a formalism used successfully to model protocols for distributed systems, namely *multi-agent systems*. We explore the exact relationship between these two frameworks here. It turns out that a key difference is the handling of agents, which are unspecified in strand spaces and explicit in multi-agent systems. We provide a family of translations from strand spaces to m ...

**Keywords:** Agents, expressiveness, multi-agent systems, security protocols, strand spaces

53 Session 1B: bidding and bargaining agents I: Coordination mechanisms for dependency relationships among multiple agents

Wei Chen, Keith S. Decker

July 2002 **Proceedings of the first international joint conference on Autonomous agents and multiagent systems: part 1**

Full text available:  pdf(78.98 KB) Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

A recent observation about multiagent coordination is that one can describe possible mechanisms in a domain-indepen\-dent way, as simple or complex responses to certain dependency relationships between the activities of different agents. Thus agent programmers can separate encoding agent domain actions from the solution to particular coordination problems. This paper explores the specification of a large range of coordination mechanisms for the common hard enablement relationship between tasks at ...

**Keywords:** coordinating multiple agents and multiple activities, coordination infrastructures

54 Military applications: Anticipatory Planning Support System

John R. Surdu, John M. D. Hill, Udo W. Pooch

December 2000 **Proceedings of the 32nd conference on Winter simulation**

Full text available:  pdf(215.81 KB) Additional Information: [full citation](#), [abstract](#), [references](#)

A new approach to military planning and execution has been proposed. This approach seeks to merge planning and execution, and replaces reaction to events with anticipation of events. This paper presents a methodology for building an automated system to support Anticipatory Planning. A Plan Description is developed to manage the many tree-like branches that occur in planning and execution of an operation. A Planning Executive can use the differences between the plan and the actual operation to co ...

55 The elements of computer credibility

B. J. Fogg, Hsiang Tseng

May 1999 **Proceedings of the SIGCHI conference on Human factors in computing systems: the CHI is the limit**

Full text available:  pdf(1.07 MB) Additional Information: [full citation](#), [abstract](#), [references](#), [citations](#), [index terms](#)

Given the importance of credibility in computing products, the research on computer credibility is relatively small. To enhance knowledge about computers and credibility, we define key terms relating to computer credibility, synthesize the literature in this domain, and propose three new conceptual frameworks for better understanding the elements of computer credibility. To promote further research, we then offer two perspectives on what computer users evaluate when assessing credibil ...

**Keywords:** captology, credibility, expertise, influence, information quality, persuasion, psychology of HCI, trust, trustworthiness

56 A sustainable fishing simulation using mathematical modeling and database access through the World Wide Web

Vineet Kapur, Douglas Troy, James Oris  
October 1997 **Crossroads**, Volume 4 Issue 1

Full text available:  [html\(31.74 KB\)](#) · Additional Information: [full citation](#), [index terms](#)



57 Technical papers: requirements engineering: Requirements, domain and specifications: a viewpoint-based approach to requirements engineering

Andrés Silva  
May 2002 **Proceedings of the 24th International Conference on Software Engineering**


Full text available:  [pdf\(1.17 MB\)](#) · Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Viewpoint-based Requirements Engineering (VBRE) is based on the fact that there is a multiplicity of stakeholders that take part in any requirements process. This will inevitably lead to conflicts and inconsistencies that, if adequately managed, can be used to improve the process, as they are sources of requirements. There comes a time in every VBRE process when different viewpoints need to be compared to find discrepancies (conflicts, inconsistencies). But in Requirements Engineering (RE) we also ...



58 Discovering the secrets of DNA

Peter Friedland, Laurence H. Kedes  
November 1985 **Communications of the ACM**, Volume 28 Issue 11

Full text available:  [pdf\(2.12 MB\)](#) · Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#), [review](#)

Sophisticated software tools are becoming increasingly important in helping biologists understand how nature operates. Symbolic pattern-recognition and artificial-intelligence methodologies are contributing to the development of such software.



59 Efficient identification of Web communities


Gary William Flake, Steve Lawrence, C. Lee Giles  
August 2000 **Proceedings of the sixth ACM SIGKDD international conference on Knowledge discovery and data mining**

Full text available:  [pdf\(273.37 KB\)](#) · Additional Information: [full citation](#), [references](#), [citations](#), [index terms](#)



60 Clustering: Document clustering via adaptive subspace iteration

Tao Li, Sheng Ma, Mitsunori Ogihara  
July 2004 **Proceedings of the 27th annual international conference on Research and development in information retrieval**

Full text available:  [pdf\(181.80 KB\)](#) · Additional Information: [full citation](#), [abstract](#), [references](#), [index terms](#)

Document clustering has long been an important problem in information retrieval. In this paper, we present a new clustering algorithm  $ASI^1$ , which uses explicit modeling of the subspace structure associated with each cluster.  $ASI$  simultaneously performs data reduction and subspace identification via an iterative alternating optimization procedure. Motivated from the optimization procedure, we then provide a novel method to determine the number of clusters. We also discuss ...



**Keywords:** adaptive subspace identification, alternating optimization, document clustering, factor analysis

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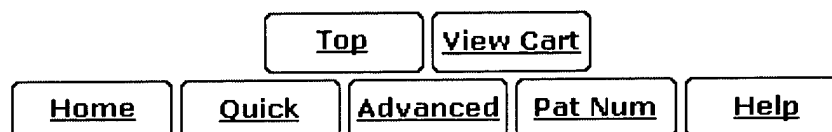
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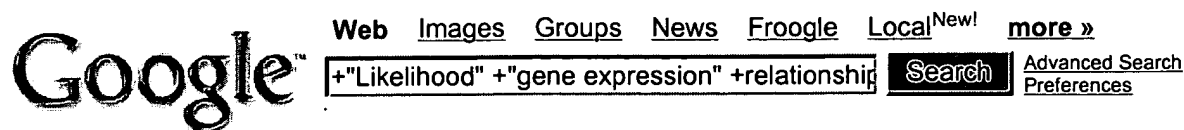
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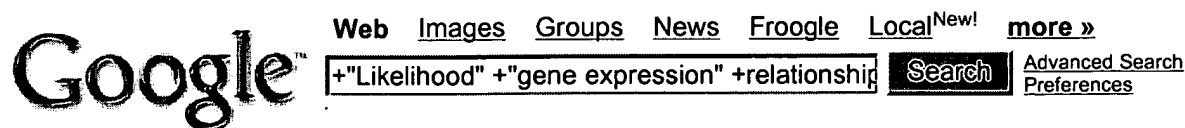
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-to define the **relationship** between the ... an **agent** and the **likelihood** of a ...  
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... mapped back to elucidate their **relationship** to the .... DNA sequence, indicating the  
**likelihood** of identifying ..... and codon redefinition utilized for **gene expression**.  
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divergence — Codon ..... Hughes 1994), novel **gene expression** patterns (Force ...  
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... in the invertase assays of this study at low w . But there was little **likelihood**  
for additional .... The **relationship** between **gene expression** and mRNA ...  
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... the null hypothesis that no **relationship** exists between ..... was an estimate of the **likelihood**  
that the ..... by Interstudy Validation of Prostate Cancer **Gene Expression**.

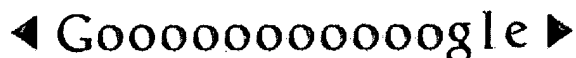
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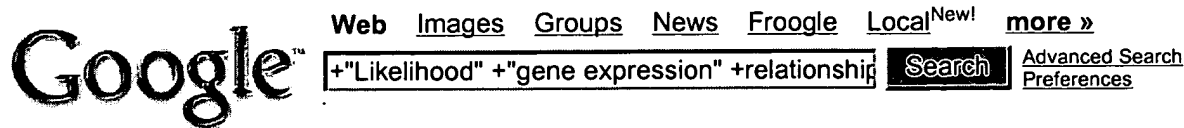


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... a large number of male partners have increased **likelihood** ..... not only of viral **gene expression**, but also ..... but epidemiological findings suggest a **relationship** to an ...

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**Research**

... questions: (1.) How does the **relationship** between education and the **likelihood** of marriage .... another, and tissues whose **gene expression** patterns are ...

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... is linked and associated with intra-tumoral **gene expression**. ... should have a high **likelihood** of responding .... see if there is any **relationship** between polymorphism ...

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... in this study was in all **likelihood** also reflective .... in CVF and its **relationship** to the ..... a persistent upregulation in collagen **gene expression**; however, because ...

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... research should clarify the **relationship** between the ..... acid-dependent gene chemistry" to improve **gene expression**. ..... more stable, with less **likelihood** of producing ...

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